



SEQUENCE LISTING

<110> Aharoni, Asaph
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O'Connell, Ann P.

<120> Fruit Flavour Related Genes And Use Thereof

<130> 160721

<140> pct/nl99/00737

<141> 1999-12-02

<150> EP 98204018.0

<151> 1998-12-02

<150> EP 99200739.3

<151> 1999-03-12

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<170> PatentIn Ver. 2.1

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Thr Ile Lys Pro Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu

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acc ctc ctg gac cag ctc act cct ccg gcg tat gtc ccc atc gtg ttc 147			
Thr Leu Leu Asp Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe			
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ttc tac ccc att act gac cat gac ttc aat ctt cct caa acc cta gct 195			
Phe Tyr Pro Ile Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala			
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gac tta aga caa gcc ctt tcg gag act ctc act ttg tac tat cca ctc 243			
Asp Leu Arg Gln Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu			
65	70	75	
tct gga agg gtc aaa aac aac cta tac atc gat gat ttt gaa gaa ggt 291			
Ser Gly Arg Val Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly			
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gtc cca tac ctt gag gct cga gtg aat tgt gac atg act gat ttt cta 339			
Val Pro Tyr Leu Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu			
95	100	105	
agg ctt cgg aaa atc gag tgc ctt aat gag ttt gtt cca ata aaa cca 387			
Arg Leu Arg Lys Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro			
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ttt agt atg gaa gca ata tct gat gag cgt tac ccc ttg ctt gga gtt 435			
Phe Ser Met Glu Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val			
125	130	135	140
caa gtc aac gtt ttc gat tct gga ata gca atc ggt gtc tcc gtc tct 483			
Gln Val Asn Val Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser			
145	150	155	
cac aag ctc atc gat gga gga acg gca gac tgt ttt ctc aag tcc tgg 531			
His Lys Leu Ile Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp			
160	165	170	
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Gly Ala Val Phe Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu			
175	180	185	
tct gaa gca gca ttg ctt ttc cca ccg aga gat gac ttg cct gaa aag 627			

Ser Glu Ala Ala Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys
190 195 200

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Tyr Val Asp Gln Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala
205 210 215 220

aca agg aga ttt gta ttt ggt gtg aaa gcc ata tct tca att caa gat 723
Thr Arg Arg Phe Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp
225 230 235

gaa gcg aag agc gag tcc gtg ccc aag cca tca cga gtt cat gcc gtc 771
Glu Ala Lys Ser Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val
240 245 250

act ggt ttt ctc tgg aaa cat cta atc gct gct tct cgg gca cta aca 819
Thr Gly Phe Leu Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr
255 260 265

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Ser Gly Thr Thr Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn
270 275 280

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Leu Arg Thr Arg Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly
285 290 295 300

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Asn Leu Phe Trp Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr
305 310 315

cca gag atc agt gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat 1011
Pro Glu Ile Ser Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn
320 325 330

gga tct gtc aaa caa tgt aac ggt gat tac ttt gag act ttc aag ggt 1059
Gly Ser Val Lys Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly
335 340 345

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Lys Glu Gly Tyr Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr
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 Met Ser Ser Met Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp
 365 370 375 380

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 Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp
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 400 405 410

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 415 420 425

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 430 435 440

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 Leu Ala Ser Pro Lys Thr Leu Ile
 445 450

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taaaatgcaa gtatgataga cttgtctac gtatgttacc cgaatgtgtt tccatatgct 1521

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caca atg aaa att cac gtt aag gag tca aca att ata cgc cct gct caa 169

Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln

1 5 10 15

gaa aca ccc aag cat cgc cta caa ata tcc gac cta gac atg att gtg 217

Glu Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val

20 25 30

cca tcc aat tac gtt ccc agt gtg tat ttc tat cgg cgg tcc agt gac 265

Pro Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp

35 40 45

tgc acc gat ttt ttt gaa gtt ggt ttg ctg aag aag gct ctg agc gaa 313

Cys Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu

50 55 60

ggt ctt gtg cgg ttt tac ccc gtt gcc gga agg ttg cag aag gat gaa 361

Val Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu

65 70 75

aat cgc aaa att gag att cta tgt aac gga gag gga gtt ttg ttt ctg 409

Asn Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu

80 85 90 95

gag gcc gaa aca agt tgt ggt att gat gat ttc ggt gac ttc tca caa 457

Glu Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln

100 105 110

ggc tcg aaa ctc ctg acg ctt gtt cca act gtt ggt gat aca aag gat 505

Gly Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp

115 120 125

ata tcc tcc cat cca ctc ttg atg gca cag gta act tat ttc aaa tgt 553

Ile Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys

130 135 140

gga ggc gtt tgt gtt gga act aga gtg aat cat aca ctg gta gat gga 601
 Gly Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly
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gct tca gcg tac cat atc atc aac tca tgg gcg gag acg acg cgt ggc 649
 Ala Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly
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gtt cct att agc act caa cca ttc tat gat cgg acc ata ctg agt gtt 697
 Val Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val
 180 185 190

ggg gtt cca act tct ccc aaa ttc cat cac att gaa tat gac ccg cct 745
 Gly Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro
 195 200 205

cct tcc atg aac gct cct cct acc caa aat cct gaa atc att tct acc 793
 Pro Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr
 210 215 220

gca atc ctt aac cta tca ctt gat caa atc cac acc ctc aaa gag aaa 841
 Ala Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys
 225 230 235

tct aag aca gat cat gaa ccc aac gtc aag tat agt agg atg gcg atc 889
 Ser Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile
 240 245 250 255

cta gca gca cat atc tgg cgt agc atg tgt aaa gcg cgc gga tta tct 937
 Leu Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser
 260 265 270

gat gat caa gtt agc aag tta cac ttt cct aca gac gga cga cag aga 985
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 275 280 285

ttg aat cca cca ctc ccg cct gga tat ttt gga aat gta att ttc acc 1033
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 290 295 300

acg tcg ttg acg gct tca tcg ggt gat atc cta agt gaa cca ttg aat 1081
 Thr Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn
 305 310 315

cat act gtt gaa aga att caa aaa gca tta aag cgg atg gac gat gag 1129
 His Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu
 320 325 330 335

tat ttg aaa tca gca ctt gct tac cta aag caa cag cct gat tta aat 1177
 Tyr Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn
 340 345 350

gct cta cgg aaa gga ggc cac att tac aag tgc cct aac ctc aat atc 1225
 Ala Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile
 355 360 365

gtc aat ttg gca aat atg cca atg tat gtt gcg aat ttt gga tgg ggc 1273
 Val Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly
 370 375 380

cag ccg ata ttt gcg agg atc gtt aac aca tat tat gaa ggg ata gca 1321
 Gln Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala
 385 390 395

cat att tat cca agt ccg agc aat gat ggg acc ttg tca gtg gtt ata 1369
 His Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile
 400 405 410 415

aac tcg gta gcc gat cac atg cag ctg ttc aag aag ttc ttt tac gag 1417
 Asn Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu
 420 425 430

atc ttt gat taaggtatga aagacctagg tattttatat ttctagaaa 1466
 Ile Phe Asp

tgctactttt tttttttt tttttgggg gcgcaaatgt tgtcttactt ggaattttat 1526

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Arg Gln Lys Val Leu Leu Asp His Leu Arg Pro Ser Ser Ser Ser Asp

10 15 20

gac tct tct ctc tcc gcg tgc gta tgt gcg gct ggg gat agc gct gcg 150

Asp Ser Ser Leu Ser Ala Ser Val Cys Ala Ala Gly Asp Ser Ala Ala

25 30 35

tat gct agg aat cat gtc ttt ggg gac gat gtc gtc atc gtt gca gct 198

Tyr Ala Arg Asn His Val Phe Gly Asp Asp Val Val Ile Val Ala Ala

40 45 50

ttt cgc act cca ctc tgc aag gct aag cgt ggc ggc ttc aag tat act 246

Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg Gly Gly Phe Lys Tyr Thr

55 60 65 70

tat gct gat gat ctc ctc gca cct gtc ctc aag gcc gtg gtt gag aaa 294

Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu Lys Ala Val Val Glu Lys

75 80 85

acc aat ctc aat ccc aag gaa gtc ggg gat att gtt gtc ggt acc gtc 342

Thr Asn Leu Asn Pro Lys Glu Val Gly Asp Ile Val Val Gly Thr Val

90 95 100

ttg gcc cca gga tct cag aga gct agc gaa tgc agg atg gct gct ttc 390

Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu Cys Arg Met Ala Ala Phe

105 110 115

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Tyr Ala Gly Phe Pro Glu Thr Val Pro Val Arg Thr Val Asn Arg Gln

120 125 130

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 Cys Ser Ser Gly Leu Gln Ala Val Ala Asp Val Ala Ala Ala Ile Arg
 135 140 145 150

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 Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala Gly Leu Glu Ser Met Thr
 155 160 165

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 170 175 180

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 Asn Val Ala His Arg Phe Gly Val Ser Arg Gln Glu Gln Asp Gln Ala
 200 205 210

gca gtt gac tct cat aga aag gca gct gct gct gct gct ggt aga 726
 Ala Val Asp Ser His Arg Lys Ala Ala Ala Ala Ala Ala Gly Arg
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 235 240 245

tct ggt gat gag aaa cct gtt aca atc tct gtt gat gat ggg att cga 822
 Ser Gly Asp Glu Lys Pro Val Thr Ile Ser Val Asp Asp Gly Ile Arg
 250 255 260

aac aca aca ttg gcg gac cta gca aag ctg aag cct gtg ttt aag aaa 870
 Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu Lys Pro Val Phe Lys Lys
 265 270 275

gat ggg acc acc act gct ggt aat tct agt caa gtt agt gat ggt gct 918
 Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser Gln Val Ser Asp Gly Ala
 280 285 290

gga gct gtt ctc ttg atg aag aga agt gtt gcc gac caa aaa gga ttg 966
 Gly Ala Val Leu Leu Met Lys Arg Ser Val Ala Asp Gln Lys Gly Leu
 295 300 305 310

ccg att ctt ggt gta ttc agg aat ttt gtt gct gtt ggt gtg gat cct 1014
 Pro Ile Leu Gly Val Phe Arg Asn Phe Val Ala Val Gly Val Asp Pro
 315 320 325

gcc atc atg ggt gtt ggc cca gct gct gca att cca gtt gca gtt aag 1062
 Ala Ile Met Gly Val Gly Pro Ala Ala Ala Ile Pro Val Ala Val Lys
 330 335 340

gca gct ggt tta gag ctt gat gat att gac ctt ttt gag ata aat gag 1110
 Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp Leu Phe Glu Ile Asn Glu
 345 350 355

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 360 365 370

cca gaa aaa atc aat gtt aac gga ggt gca atg gcc atc ggc cat cca 1206
 Pro Glu Lys Ile Asn Val Asn Gly Gly Ala Met Ala Ile Gly His Pro
 375 380 385 390

ctt ggt gca aca ggt gcc cgg tgt gtt gcc act ctt ttg cat gag atg 1254
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 395 400 405

aag cgt cgt ggt aaa gac tgc cgc tat gga gtg atc tca atg tgc ata 1302
 Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly Val Ile Ser Met Cys Ile
 410 415 420

ggc aca ggg atg ggt gca gcc gct gtt ttt gaa aga gga gac cgg acc 1350
 Gly Thr Gly Met Gly Ala Ala Ala Val Phe Glu Arg Gly Asp Arg Thr
 425 430 435

gat gaa ctc tgc aat gct cgc aag gtt gaa tca ctc aac ttc tta tcc 1398
 Asp Glu Leu Cys Asn Ala Arg Lys Val Glu Ser Leu Asn Phe Leu Ser
 440 445 450

aag gat gtt cgg tagtagagaa tggtagtga caggagctat tccaatcaat 1450
 Lys Asp Val Arg
 455

aatgtttggt ggagtctgaa aatcatagta aagcactgga ataacgttgc taagttttc 1510

gttgggtact accttggtta ttgggatgga atacacatgt agttgggttg ttctcccaga 1570

cctcccactt gttggcatat tcatttttgt ccaacctaaa aagttccatt ttataggact 1630

tcatttcaat aacattgggt ttgcgccact aaagcagtgc ctaaaactgt aattgggtaa 1690

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Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys

1 5 10

aaa acc gag aac cac gac gtc ggt tgt tta cca aac agc gcc acc tcc 158

Lys Thr Glu Asn His Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser

15 20 25

acc gtt caa aac tca gtc cct tcc acc tcc ctc agc tcc gcc gac gcc 206

Thr Val Gln Asn Ser Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala

30 35 40

acc ctc ggc cgc cac ctg gca cgc cgc ctc gtt caa atc ggc gtc acc 254

Thr Leu Gly Arg His Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr

45 50 55

gac gtc ttc acc gtc ccc ggc gac ttc aac ttg acc ctt ctt gac cac 302

Asp Val Phe Thr Val Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His

60 65 70 75

ctc atc gcc gag ccc ggc ctc acc aac att ggc tgc tgc aac gag ctc 350
 Leu Ile Ala Glu Pro Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu
 80 85 90

aac gcc ggg tac gcc gcc gac ggc tac gcg cgg tcg cgt ggc gtc ggc 398
 Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly
 95 100 105

gcg tgc gtg gtg act ttc act gtt ggt gga ctg agt gtg ctg aac gcg 446
 Ala Cys Val Val Thr Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala
 110 115 120

atc gcc ggc gcg tat agt gag aat ttg ccg gtg att tgt att gtt ggt 494
 Ile Ala Gly Ala Tyr Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly
 125 130 135

ggg ccc aac tct aac gat tat ggg act aac cgg att ctt cac cat act 542
 Gly Pro Asn Ser Asn Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr
 140 145 150 155

att ggg ttg ccg gac ttc agt caa gag ctc cgg tgc ttt cag acc gtg 590
 Ile Gly Leu Pro Asp Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val
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 Thr Cys Phe Gln Ala Val Val Asn Asn Leu Glu Asp Ala His Glu Met
 175 180 185

att gat act gca att tcg act gcg ttg aaa gaa agc aag cct gtg tat 686
 Ile Asp Thr Ala Ile Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr
 190 195 200

atc agc att ggc tgc aac ttg gct ggg att cct cat cct act ttc agc 734
 Ile Ser Ile Gly Cys Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser
 205 210 215

cgt gaa cct gtt cca ttt tca ttg tct cca aaa ttg agc aat aag tgg 782
 Arg Glu Pro Val Pro Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp
 220 225 230 235

gga tta gag gct gca gtg gag gct gct gca gag ttc ttg aac aag gca 830
 Gly Leu Glu Ala Ala Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala
 240 245 250

gtg aag cca gtt atg gtg ggc ggg ccc aaa ctg cgc tct gca cat gct 878
 Val Lys Pro Val Met Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala
 255 260 265

ggt gat gcc ttt gtt gaa ctg gct gat gct tct gga ttt gct ctg gct 926
 Gly Asp Ala Phe Val Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala
 270 275 280

gtg atg cca tca gca aag ggg caa gtg cca gag cac cac ccc cat ttc 974
 Val Met Pro Ser Ala Lys Gly Gln Val Pro Glu His His Pro His Phe
 285 290 295

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 Ile Gly Thr Tyr Trp Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile
 300 305 310 315

gtg gag tct gca gat gca tac ttg ttt gct ggg ccg att ttc aat gac 1070
 Val Glu Ser Ala Asp Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp
 320 325 330

tac agc tca gtt ggg tac tcg ctc ctt ctc aag aaa gag aag gcg atc 1118
 Tyr Ser Ser Val Gly Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile
 335 340 345

att gtg cag cca gat cgt gtg acg ata ggg aat ggc cct aca ttt ggt 1166
 Ile Val Gln Pro Asp Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly
 350 355 360

tgt gtt ctc atg aag gat ttc ctc tta ggc cta gca aag aag ctg aag 1214
 Cys Val Leu Met Lys Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys
 365 370 375

cat aac aac act gct cat gag aac tac cgc agg atc ttt gtg cct gat 1262
 His Asn Asn Thr Ala His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp
 380 385 390 395

ggc cac cct ctg aag gct gca ccc aaa gaa cct ttg agg gtt aat gtt 1310
 Gly His Pro Leu Lys Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val
 400 405 410

ctg ttc aaa cac att cag aat atg ctg tca gct gaa acc gct gtg att 1358
 Leu Phe Lys His Ile Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile
 415 420 425

gct gag aca ggg gac tca tgg ttt aac tgt cag aag ctg aaa ttg cca 1406
 Ala Glu Thr Gly Asp Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro
 430 435 440

ccc ggc tgc ggg tat gag ttc caa atg caa tat gga tca att ggt tgg 1454
 Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp
 445 450 455

tca gtt gga gca act ctt ggg tat gct cag gct gta cct gag aag cga 1502
 Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg
 460 465 470 475

gtg att tct ttc att ggt gat ggg agc ttc cag gtg act gct caa gat 1550
 Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp
 480 485 490

gtg tcc aca atg att cga aat gga cag aga acc att att ttc ctg ata 1598
 Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile
 495 500 505

aac aat ggt gga tac acc att gaa gtg gaa atc cat gat gga cca tac 1646
 Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr
 510 515 520

aat gtg atc aag aac tgg aac tac act gga ctg gtt gat gca atc cac 1694
 Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His
 525 530 535

aat ggg gaa ggc aag tgc tgg aca acc aag gtg cgt tgc gaa gag gag 1742
 Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu
 540 545 550 555

ctg att gaa gca ata gag act gca aat gga ccc aag aag gat agc ttc 1790
 Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe
 560 565 570

tgc ttc att gag gtg att gtt cac aag gat gat acc agc aaa gag ttg 1838
 Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu
 575 580 585

ctt gag tgg ggg tct agg gtt tct gct gcc aac agc cgc cca cct aat 1886
 Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn
 590 595 600

cct cag taaaactctc ctgtgtcata tgaaggcctt cattcacatt cacagattta 1942

Pro Gln

605

gatcaagcca agctcttgtg caaattttcc ttatgtttt cctgtcaact ggagaatggt 2002

gtctgtcaag tttttttac actacagtga tttctggtt gtctgtatat ttccttctga 2062

atattagtat ctcttgattt ttcaattgat caaattctgt gatcctaaat ggtttgtgga 2122

aaaaaaaaa aaaaaaaaaa

2141

<210> 5

<211> 1415

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (56)..(1054)

<223> cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 5

taatctagct tctgcaccaa aactatcaga taattaagaa tctgccacag agaaa atg 58

Met

1

gtg atg tct atc gag cag gaa cac ccc aag aag gca tct gga tgg gct 106

Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp Ala

5

10

15

gca aga gat tca tct ggt gtt ctc tct ccc ttc agt ttc tcc aga agg 154

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg Arg

20

25

30

gaa acc gga gag aaa gac gtg acg ttc aaa gtg atg tac tgt ggg att 202

Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly Ile

35

40

45

tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 250

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
 50 55 60 65

tat cct ctg gtt cca ggg cat gag att gtt ggt gaa gtg acg gaa gta 298
 Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
 70 75 80

gga agc aat gta caa aaa ttc aaa gtt gga gac aga gtc ggt gtt gga 346
 Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
 85 90 95

tgc att gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 394
 Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
 100 105 110

gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 442
 Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
 115 120 125

gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gat 490
 Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
 130 135 140 145

gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggt gct 538
 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
 150 155 160

gcg ccg etc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 586
 Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
 165 170 175

ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc 634
 Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
 180 185 190

ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag 682
 Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
 195 200 205

gtt aca gtg att agt aca tcc cct aag aaa gag gag gaa gct cgt aaa 730
 Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg Lys
 210 215 220 225

cac cta gga gct gac tcg ttt ttg gtt agc cgt gac caa gat caa atg 778
 His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met
 230 235 240

cag gct gcc att ggt acc atg gat ggg atc att gac acg gtt tct gca 826
 Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
 245 250 255

caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag 874
 Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
 260 265 270

ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctg cca gtt ttt 922
 Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
 275 280 285

cct tta ctc atg gga aga aag atg gta gct ggt agc ggc att ggg ggt 970
 Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly Gly
 290 295 300 305

atg aag gag aca caa gag atg ata gat ttt gca gcc aag cac aac att 1018
 Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn Ile
 310 315 320

aca gca gac atc gaa gtc ata cca atc gac tac ttg taacactgct 1064
 Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330

atggagcgtc tagtcaaagc agatgtcaga taccgttttg tcatcgacat tggaacaca 1124

ctgaaggcta gctcttaaat tctgcaatcc agactggatc aatgaagaaa caagaacaga 1184

aacggagact gatttagtgt catactcggg gttggttttc ctgtagcat ttttgttgt 1244

ctgctacatg aataatgatc acatgaacaa ctgccttctg tgatgatttg ataataaaag 1304

aatacatgaa caatgatact gccttctttt gtaatgtttt ttactatata atcatttcaa 1364

attattttgc tatatctcta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1415

<210> 6
 <211> 452
 <212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol acyl transferase

<400> 6

Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His Thr Ile Lys Pro

1 5 10 15

Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp

20 25 30

Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile

35 40 45

Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln

50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val

65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu

85 90 95

Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys

100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu

115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val

130 135 140

Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile

145 150 155 160

Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe

165 170 175

Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala

180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln

195 200 205

Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe
210 215 220

Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu
245 250 255

Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg
275 280 285

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
290 295 300

Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
340 345 350

Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
355 360 365

Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
370 375 380

Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
385 390 395 400

Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
405 410 415

Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
420 425 430

Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro

435 440 445
 Lys Thr Leu Ile
 450

 <210> 7
 <211> 663
 <212> DNA
 <213> Fragaria x ananassa

 <220>
 <221> CDS
 <222> (3)..(545)
 <223> partial cDNA

 <220>
 <223> Strawberry alcohol dehydrogenase

 <400> 7
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 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu
 1 5 10 15

 gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His
 20 25 30

 cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg 143
 His Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu
 35 40 45

 gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa 191
 Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln
 50 55 60

 atg caa gag get atg gac tca ctg gat tac att att gac acc att cca 239
 Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro
 65 70 75

 gtg ttc cac cct ctt gag cct tac ctc tct ttg ttg aag ctt gat ggg 287
 Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly

80	85	90	95
----	----	----	----

aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct 335
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser
100 105 110

cca ttg gtc atg ctt ggg gag gaa gac gat cac cgg gag ctt tgt ggg 383
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly
115 120 125

gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga 431
Glu His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg
130 135 140

gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct 479
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala
145 150 155

ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat 527
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp
160 165 170 175

tgt tgc cgg cag caa tct tgatcaataa gaaagaaaga aggcatcatc 575
Cys Cys Arg Gln Gln Ser
180

gagtgtgtc ctattttat cgagtactct gtctcatctt atcttaaaca atataaataa 635

acaaagaaaa aaaaaaaaaa aaaaaaaa 663

<210> 8
<211> 694
<212> DNA
<213> Fragaria x ananassa

<220>
<221> CDS
<222> (1)..(528)
<223> partial cDNA

<220>
<223> Strawberry alcohol dehydrogenase

<400> 8
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 Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
 1 5 10 15

 tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca 96
 Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

 tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca 144
 Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

 gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg 192
 Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

 ctt tat aca gga gct gtt gcc tat ggt gca tgt tcg gca gca ctg cag 240
 Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
 65 70 75 80

 cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg 288
 Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

 gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag 336
 Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

 tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg 384
 Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125

 ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata 432
 Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140

 tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt 480
 Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
 145 150 155 160

 gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg 528
 Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met

165 170 175

tgattcttgc tcctattata tcctcctage cattattage tacttaggtt tgttcatact 588

tcataggtga actcattage tattcttaca ttgttcctt atgaataaag aagtcaagat 648

tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 694

<210> 9

<211> 1586

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (78)..(1268)

<223> cDNA

<220>

<223> Strawberry aminotransferase

<400> 9

aaaccgtcgg cgtctgtaaa tgcgtcgccg ctccggagaa gacagagtac aagactcagg 60

tgaatcgcaa tgccaac atg gcc aag ctt caa gcc ggt tat ctt ttt cca 110

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro

1 5 10

gag att gcg agg agg agg aat gcg cac ttg cag aag cac cct gat gcg 158

Glu Ile Ala Arg Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala

15 20 25

aag ata att cca ctt gga att ggt gat act acc gag cca att cca gaa 206

Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu

30 35 40

tat ata acc tct gca atg gca aag aga gca ctt gcc atg tcc acc cta 254

Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu

45 50 55

gag ggt tac agt ggt tat gga cct gaa caa ggt gaa aag cca ctg aga 302

Glu Gly Tyr Ser Gly Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg

60 65 70 75

gtt gca att gct aaa acg ttt tat ggc gac ctt ggc ata gag gaa gat 350
Val Ala Ile Ala Lys Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp
80 85 90

gac ata ttt gtt tct gat ggg gca aaa tgt gac ata tcc cgc ctt cag 398
Asp Ile Phe Val Ser Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln
95 100 105

gtt ctt ttt ggg gcg gat aaa aca ata gca gtg caa gat cca tcg tat 446
Val Leu Phe Gly Ala Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr
110 115 120

ccg gct tat gta gac tca agt gtt att atg ggc cag aca gga cag tat 494
Pro Ala Tyr Val Asp Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr
125 130 135

cag aaa tct gtt cag aag ttt gga aac atc gag tac atg agg tgt act 542
Gln Lys Ser Val Gln Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr
140 145 150 155

ccc gat aat gga ttt ttt cct gat ctg tcc tct act aag cga aca gat 590
Pro Asp Asn Gly Phe Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp
160 165 170

atc ata ttt ttc tgt tca cca aac aat cct act ggt tct gct gca aca 638
Ile Ile Phe Phe Cys Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr
175 180 185

agg gag caa ctg aca caa ctt gta aag ttt gcc aag gat aat ggt tca 686
Arg Glu Gln Leu Thr Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser
190 195 200

atc ata gtc tat gat tct gca tat gcc atg tat atg tca gat gat aat 734
Ile Ile Val Tyr Asp Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn
205 210 215

cca cgc tcc atc ttt gaa atc cct gga gct aaa gat gtt gca ctt gag 782
Pro Arg Ser Ile Phe Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu
220 225 230 235

aca tca tca ttt agt aag tat gcc gga ttc act gga gtt cgt ttg ggg 830
Thr Ser Ser Phe Ser Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly
240 245 250

tgg act gtg gtt cca aag cag ttg cag tat tca gat ggt ttt caa gtt 878
 Trp Thr Val Val Pro Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val
 255 260 265

gcc aag gat ttc aac cgc att gtt tgt act tgc ttc aat ggt gca tcc 926
 Ala Lys Asp Phe Asn Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser
 270 275 280

act att atc caa gct ggt ggt ctg gct tgc ctt caa cca aag ggt gtt 974
 Thr Ile Ile Gln Ala Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val
 285 290 295

aag gct atg cac ggt gtg ata aat ttc tac aaa gaa aat act aag atc 1022
 Lys Ala Met His Gly Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile
 300 305 310 315

ata atg gag acg ttt aac tct ctt ggc ttt aac gtg tat gga ggg aca 1070
 Ile Met Glu Thr Phe Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr
 320 325 330

aac gct cca tat gtg tgg gtc cac ttc cct gga caa agc tcc tgg gat 1118
 Asn Ala Pro Tyr Val Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp
 335 340 345

gtg ttt gct gag atc ctt gag aag act cat gtg gta acc aca cct gga 1166
 Val Phe Ala Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly
 350 355 360

agt ggc ttt gga cct ggt ggt gaa ggt ttc atc agg gta agt gcc ttt 1214
 Ser Gly Phe Gly Pro Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe
 365 370 375

gga cac agg aaa aat ata tta gaa gca tgt aaa aga ttc aag caa tta 1262
 Gly His Arg Lys Asn Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu
 380 385 390 395

tac aag tgaggactgc ggatctgaat ttagaccag ttctactgc atgctagtgt 1318
 Tyr Lys

aacctatttg cctcccatgt ccgttctatg ctaaatattt tagcacgttc caattccgta 1378

ttcagtttgt cggctttagt ttatgaatta tggagatttt agctattgta aaaatgattc 1438

gatcagcctt gtttcatgt gttacactta attgttgtaa catttgtag gatcagaagc 1498

tttgattctg ttgctagaa tagtataatt ttacctaat aaagtgggtg atctttctg 1558

gcctgcaaaa aaaaaaaaaa aaaaaaaaaa 1586

<210> 10

<211> 1471

<212> DNA

<213> Cucumis melo

<220>

<221> CDS

<222> (1)..(1368)

<223> cDNA

<220>

<223> Honey dew melon alcohol acyl transferase

<400> 10

atg gac ttc tct ttt cac gta cga aaa tgc caa cca gaa ttg att gca 48
Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
1 5 10 15

cca gca aat cct aca ccc tat gaa ttt aaa caa ctt tct gat gtg gat 96
Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
20 25 30

gat caa caa agc tta agg ctt caa ttg cca ttc gta aat atc tat ccc 144
Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
35 40 45

cat aat cca agt ttg gag gga aga gat cca gtg aag gta ata aag gaa 192
His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
50 55 60

gca att gga aag gcg ttg gtg ttc tac tat cct tta gca gga aga ttg 240
Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
65 70 75 80

aga gaa ggg cca ggt aga aag ctt ttt gtt gaa tgt aca ggt gaa gga 288
Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
85 90 95

atc ttg ttt att gaa gcg gat gca gat gtg agc tta gaa gaa ttt tgg 336
 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110

gat act ctt cca tat tca ctt tca agc atg cag aac aat att ata cat 384
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125

aac gct tta aat tct gat gaa gtc ctc aat tct cca tta ttg ctc att 432
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
 130 135 140

cag gtg aca cga ctc aag tgt gga ggt ttc att ttt ggt ctt tgt ttc 480
 Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
 145 150 155 160

aat cat act atg gca gat ggt ttt ggt att gtc caa ttc atg aag gct 528
 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
 165 170 175

aca gcg gag ata gct cgt gga gct ttt gct cca tct att tta cca gta 576
 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
 180 185 190

tgg caa aga gct ctc tta acc gca aga gac cct ccc aga atc act ttt 624
 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe
 195 200 205

cgc cac tat gaa tac gac caa gta gtc gac atg aag agc ggc ctc att 672
 Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile
 210 215 220

cca gtc aat agc aag atc gat caa tta ttc ttc ttt agc caa ctt caa 720
 Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln
 225 230 235 240

atc tcc acc ctt cgc caa act ttg cca gcc cac ctt cac gat tgc cct 768
 Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro
 245 250 255

tcc ttc gag gtc ctc act gcc tat gtt tgg cgc ctc cgt acc ata gcc 816
 Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala
 260 265 270

ctt caa ttt aag cca gag gag gaa gtg cgg ttt ctt tgc gta atg aat 864
 Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn
 275 280 285

cta cgc tcg aag atc gac ata cca tta ggg tat tat ggt aat gcg gta 912
 Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val
 290 295 300

ggt gtt cct gca gta atc acc acc gct gcg aag ctt tgt ggg aac cca 960
 Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro
 305 310 315 320

ctt ggt tat gct gta gac ttg att agg aag gcc aag gct aag gca acg 1008
 Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr
 325 330 335

atg gag tac ata aag tct acg gtg gat ctt atg gtg att aaa gga cga 1056
 Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg
 340 345 350

ccc tat ttc act gta gtt gga tca ttt atg atg tca gac cta acg aga 1104
 Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg
 355 360 365

att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga 1152
 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
 370 375 380

gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt 1200
 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
 385 390 395 400

tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt 1248
 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
 405 410 415

cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat 1296
 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
 420 425 430

gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg 1344
 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
 435 440 445

caa act att caa tct gct tcg aaa taaataatat tgttgaaggt gggctctgagt 1398

Gln Thr Ile Gln Ser Ala Ser Lys

450 455

tgactcgacc atatcgatgc atgcaagctt gatccggctg ctaacaaagc ccgaaaggaa 1458

gctgagttgc tgt 1471

<210> 11

<211> 1485

<212> DNA

<213> Malus sp.

<220>

<221> CDS

<222> (1)..(1362)

<223> cDNA

<220>

<223> Apple alcohol acyl transferase

<221> misc_feature

<222> (1425)..(1425)

<223> N is any nucleic acid

<400> 11

atg tca ttc tca gta ctt cag gtg aaa cga ttg caa ccg gaa ctt ata 48

Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile

1 5 10 15

act ccg gca aag tca acg cct caa gaa aca aag ttt ctc tca gat att 96

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile

20 25 30

gac gac caa gaa agc ttg aga gtt cag att cca atc ata atg tgt tac 144

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr

35 40 45

aaa gac aac cct tca ctt aat aaa aat cgt aat ccc gtt aag gca att 192

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile

50 55 60

agg gaa gcc tta agt aga gca tta gtg tat tac tac ccc tta gct gga 240

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
65 70 75 80

agg ctt agg gaa ggg cct aat aga aag ctc gtg gtc gat tgc aat ggt 288
Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
85 90 95

gaa ggt atc ttg ttc gtt gag gct tct gct gat gtc aca ctt gag caa 336
Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
100 105 110

cta gga gac aaa att cta ccc cct tgt cca ctt tta gag gag ttc tta 384
Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu
115 120 125

tat aat ttt cca ggc tct gat gga att att gat tgt cct ttg ctg ctg 432
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu
130 135 140

att cag gtg acc tgt ctt aca tgt gga ggt ttc ata ctt gca ttg cgc 480
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg
145 150 155 160

cta aac cac aca atg tgt gat gca gct gga ttg ctc ttg ttc ctg acc 528
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr
165 170 175

gcc atc gcg gag atg gca aga ggc gca cat gca cca tct att cta cca 576
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro
180 185 190

gtg tgg gag aga gag ctc ttg ttc gct cga gat cca cca aga att aca 624
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr
195 200 205

tgt gct cgt cat gaa tat gaa gac gtg att ggt cat tct gat ggc tca 672
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser
210 215 220

tac gca tcc agt aac cag tca aac atg gtt caa cga tct ttc tac ttt 720
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe
225 230 235 240

ggt gcc aag gag atg aga gtc ctt cga aaa cag att cca ccc cac cta 768
 Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu
 245 250 255

att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa 816
 Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys
 260 265 270

tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt 864
 Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val
 275 280 285

tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc 912
 Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro
 290 295 300

ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag 960
 Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys
 305 310 315 320

gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtg 1008
 Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val
 325 330 335

aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca 1056
 Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala
 340 345 350

gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt 1104
 Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser
 355 360 365

tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat 1152
 Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn
 370 375 380

ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat 1200
 Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp
 385 390 395 400

ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata 1248
 Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile
 405 410 415

ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag 1296
 Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln
 420 425 430

gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac 1344
 Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn
 435 440 445

ctt aga tca act agt caa tgatgtaagt gttaaagta atgcacttc 1392
 Leu Arg Ser Thr Ser Gln
 450

tgtaatgtag agttgtgtct cttggaactt atcncaagag ttatagctgt tatccaaagg 1452

tctgaatggt attaaaaaat agccaataat aag 1485

<210> 12
 <211> 1291
 <212> DNA
 <213> Musa sp.

<220>
 <221> CDS
 <222> (1)..(1257)
 <223> cDNA

<220>
 <223> Banana alcohol acyl transferase

<400> 12
 atg agc ttc gct gtg acc aga aca agc cgg tct ttg gtc act cca tgc 48
 Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
 1 5 10 15

ggg gtc acg ccg acg ggc tcg ctc ggc ctc tcc gcc atc gac cgg gtg 96
 Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
 20 25 30

ccc ggc ctc agg cat atg gtg cgg tcg cta cac gtg ttc agg caa ggc 144
 Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
 35 40 45

cgg gag ccg gcc agg atc atc agg gaa gca ctg tcg aag gcg ctg gtg 192

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60

aag tac tac ccc ttc gcg ggg cgg ttc gtg gac gat ccc gag ggc ggc 240
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80

ggc gag gtt cgt gtc gct tgc act ggc gag ggc gct tgg ttc gtc gag 288
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95

gcc aag gcg gac tgc agc ttg gag gac gtg aag tac ctc gat ctc ccg 336
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110

ctc atg atc cct gag gac gcg ctc ctg ccc aag ccc tgc ccg gga ctg 384
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125

aac ccc ctc gac ctc cct ctc atg ctg cag gtg aca gag ttc gtg ggc 432
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140

ggc gga ttc gtg gtc ggc ctc atc tcc gtc cat acc atc gcc gac ggc 480
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160

ctc ggc gtc gtc cag ttc atc aac gcc gtc gcc gag atc gcc cgt ggc 528
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175

ctg ccg aag ccc acc gtg gag cct gca tgg tcc cgg gag gtc ata ccc 576
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

aac cca cct aag ctg cct ccc ggt ggc ccg ccc gtg ttc ccc tcc ttc 624
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
195 200 205

aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac 672
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
210 215 220

gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc 720
Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
225 230 235 240

gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac 768
Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
245 250 255

ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc 816
Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
260 265 270

cac ctg ttg cgc cag gtc gtc ctc ctg ccc ccc gag gat ggc tac tac 864
His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
275 280 285

ggc aac tgc ttc tac ccg gtg acc gcc acc gcc cca agc ggc agg atc 912
Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
290 295 300

gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag 960
Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
305 310 315 320

tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag 1008
Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
325 330 335

gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg 1056
Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
340 345 350

gac tgg acc cgg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag 1104
Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
355 360 365

ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc 1152
Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
370 375 380

atc atc ggg gcg ccg ccg gcg ccg caa aag ggg act cgg gtg atg gcg 1200
Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
385 390 395 400

cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa 1248
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415

ggc ttc gct taaaccagca gcagtgtagt acttgcagt atcc 1291
 Gly Phe Ala

<210> 13
 <211> 1488
 <212> DNA
 <213> *Fragaria vesca*

<220>
 <221> CDS
 <222> (1)..(1365)
 <223> cDNA

<220>
 <223> *Strawberry vesca* alcohol acyl transferase

<400> 13
 atg gag aaa att gag gtc agt ata att tcc aaa cac acc atc aaa cca 48
 Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
 1 5 10 15

tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac 96
 Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
 20 25 30

cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att 144
 Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
 35 40 45

act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat 192
 Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
 50 55 60

gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc 240
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 65 70 75 80

aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt 288
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu

85	90	95	
gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa 336			
Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys			
100	105	110	
atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa 384			
Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu			
115	120	125	
gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att 432			
Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile			
130	135	140	
ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc 480			
Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile			
145	150	155	160
gat gga aga act tca gac tgt ttt ctc aag teg tgg tgt gct gtt ttt 528			
Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe			
165	170	175	
cgt ggt tct cgt gac aaa atc ata cat cct aat ctc tct caa gca gca 576			
Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala			
180	185	190	
ttg ctt ttc cca cca aga gat gac ttg cct gaa aag tat gcc cgt cag 624			
Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln			
195	200	205	
atg gaa ggg tta tgg ttt gtc gga aaa aaa gtt gct aca agg aga ttt 672			
Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe			
210	215	220	
gta ttt ggt gcg aaa gcc ata tct gta att caa gat gaa gca aag agc 720			
Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser			
225	230	235	240
gag tcc gtg ccc aag cca tca cga gtt cag gct gtc act agt ttt ctc 768			
Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu			
245	250	255	
tgg aaa cat cta atc gct act tct cgg gca cta aca tca ggt act act 816			

Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

tca aca aga ctt tct ata gca acc cag gta gtg aac ata aga tca cgg 864
Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
275 280 285

agg aac atg gag aca gtg tgg gat aat gcc att gga aac ttg ata tgg 912
Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
290 295 300

ttc gct ccg gcc ata cta gag cta agt cat aca aca cta gag atc agt 960
Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
305 310 315 320

gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat gga tct gtc aaa 1008
Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

caa tgt aac ggt gat tac ttt gag act ttc atg ggt aaa gag gga tat 1056
Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
340 345 350

gga agc atg tgc gag tat cta gat ttt cag agg act atg agt tct atg 1104
Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
355 360 365

gaa cca gca cca gag att tat tta ttc acg agc tgg act aat ttt ttc 1152
Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
370 375 380

aac caa ctt gat ttt gga tgg ggg agg aca tca tgg att gga gtt gca 1200
Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
385 390 395 400

gga aaa att gaa tct gca ttt tgc aat ctc aca aca tta gtt cca aca 1248
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
405 410 415

cca tgc gat act gga att gaa gcg tgg gtg aat cta gaa gaa gaa aaa 1296
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
420 425 430

atg gct atg cta gaa caa gat ccc cag ttt cta gca cta gca tct cca 1344
 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
 435 440 445

aag acg cta att tca aga tat tgattaagga agattatgcg gctcgtgcaa 1395
 Lys Thr Leu Ile Ser Arg Tyr
 450 455

tgtttccatt ttgttgtgat taaggcttaa attagttcac cagccaatca ataagatgca 1455

agtatgatag actcgggtcta cgtatgttat ccg 1488

<210> 14
 <211> 434
 <212> PRT
 <213> Citrus limon
 <223> Citrus limon alcohol acyl transferase

<400> 14
 Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln Glu
 1 5 10 15

Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro
 20 25 30

Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys
 35 40 45

Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu Val
 50 55 60

Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn
 65 70 75 80

Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu
 85 90 95

Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly
 100 105 110

Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile
 115 120 125

Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly
130 135 140

Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala
145 150 155 160

Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val
165 170 175

Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly
180 185 190

Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro
195 200 205

Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala
210 215 220

Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser
225 230 235 240

Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu
245 250 255

Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp
260 265 270

Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu
275 280 285

Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr
290 295 300

Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His
305 310 315 320

Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr
325 330 335

Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala
340 345 350

Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val

355 360 365
 Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln
 370 375 380
 Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His
 385 390 395 400
 Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn
 405 410 415
 Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu Ile
 420 425 430

Phe Asp

<210> 15
 <211> 1296
 <212> DNA
 <213> *Mangifera indica*

<220>
 <221> CDS
 <222> (1)..(1293)
 <223> cDNA

<220>
 <223> Mango alcohol acyl transferase

<400> 15
 atg ata atc acg gtg aag gag tcg acg atg gtc ccg ccg tcg gcg gag 48
 Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu
 1 5 10 15

acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc 96
 Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
 20 25 30

cga ttt cat act ccc agc gtt tac ttc tac cgg ccc acc ggg gcc ata 144
 Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
 35 40 45

aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg 192

Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
50 55 60

gtg ccg ttc tac cca atg gcg ggg cgg tta aag cgt gac gaa gat gga 240
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
65 70 75 80

agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc 288
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala
85 90 95

gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta 336
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu
100 105 110

gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct 384
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser
115 120 125

acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga 432
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly
130 135 140

gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct 480
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser
145 150 155 160

ggt ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat 528
Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
165 170 175

gtt aac atc acc ctg ttc att gac cgg act ctg ctc aga gca cag gat 576
Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
180 185 190

ccc cct cag cct act ttc cca cac aca tgg aat acc agg ccg cct cct 624
Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
195 200 205

tcc ctg aaa act cct cca cca gca gtt tct gag cct act gct gtc tcc 672
Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
210 215 220

att ttt aag ttg acg cgg gac cag ctc aac atc ctc aaa gcc aag gcc 720
 Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
 225 230 235 240

aaa gaa gat ggt aac act atc aac tat agc tca tat gag atg ctg gcg 768
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
 245 250 255

ggt cat gtc tgg aga tct gca tgc aag gca cgc ggc tta tct gat gat 816
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
 260 265 270

caa gag act aaa ttg tac ata gca act gac gga cgt gct aga tta atc 864
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
 275 280 285

ccc cca ctt cca cct ggt tac ttt ggg aat gtg ata ttt aca gcc aca 912
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
 290 295 300

cca atg gca gta gca ggt gat ctc cag tca aag cct ata tgg tat gct 960
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
 305 310 315 320

gct ggc cag att cat gat gcc ttg gtt cga atg gac aac gac tat tta 1008
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
 325 330 335

agg tca gcc ctc gat tac cta gag ctt cag cct gat tta tca gca tta 1056
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
 340 345 350

gtt cgt ggt gcc cat aca ttt agg tgt cca aat ctc ggg att act agt 1104
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
 355 360 365

tgg gtt aga ctg cca ata cat gat gca gat ttt ggt tgg ggt cca ccc 1152
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
 370 375 380

aca ttt atg ggg cct ggt ggg att gca tat gaa ggc tta tca ttt gta 1200
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
 385 390 395 400

ttg cca agc cct aca aat gat ggg agc tta tca gtt gcc atc tct cta 1248
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
 405 410 415

caa tct gaa cac atg aaa ctg ttt cag aag ttc ttt tat gat att taa 1296
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
 420 425 430

<210> 16
 <211> 1436
 <212> DNA
 <213> Citrus limon

<220>
 <221> CDS
 <222> (34)..(1311)
 <223> cDNA

<220>
 <223> Lemon acyl transferase

<400> 16
 atccacacta ataattcttt catatgctcg ggg atg gat ctc caa atc acc tgc 54
 Met Asp Leu Gln Ile Thr Cys
 1 5

acc gaa atc atc aag cct tct teg ccg acg cct caa cac caa agt acc 102
 Thr Glu Ile Ile Lys Pro Ser Ser Pro Thr Pro Gln His Gln Ser Thr
 10 15 20

tat aaa ctt tca att att gat caa tta act cct aat gtt tac ttt tcc 150
 Tyr Lys Leu Ser Ile Ile Asp Gln Leu Thr Pro Asn Val Tyr Phe Ser
 25 30 35

atc att ctc ttg tat tca aaa gct ggt gaa agt acc gcc aaa act tca 198
 Ile Ile Leu Leu Tyr Ser Lys Ala Gly Glu Ser Thr Ala Lys Thr Ser
 40 45 50 55

gat cac ctc aaa gaa tct ctt tca aat aca tta acc cac tac tat cct 246
 Asp His Leu Lys Glu Ser Leu Ser Asn Thr Leu Thr His Tyr Tyr Pro
 60 65 70

tta gct ggg caa ctc aaa tat gat caa ctt att gtt gat tgt aac gac 294

Leu Ala Gly Gln Leu Lys Tyr Asp Gln Leu Ile Val Asp Cys Asn Asp
75 80 85

caa ggt gtc ccg ttc atc gaa gca cac gtc acc aac gac atg cgt cag 342
Gln Gly Val Pro Phe Ile Glu Ala His Val Thr Asn Asp Met Arg Gln
90 95 100

ctt ctt aaa ata cca aat att gat gtt ctc gaa caa ctc cta cca ttc 390
Leu Leu Lys Ile Pro Asn Ile Asp Val Leu Glu Gln Leu Leu Pro Phe
105 110 115

aaa ccg cat gag ggt ttt gat tct gat cgt tcc aac cta acc gtt cag 438
Lys Pro His Glu Gly Phe Asp Ser Asp Arg Ser Asn Leu Thr Val Gln
120 125 130 135

gtc aat tac ttt ggt tgt gaa gga atg gcg att ggt ctg tgc ttc aga 486
Val Asn Tyr Phe Gly Cys Glu Gly Met Ala Ile Gly Leu Cys Phe Arg
140 145 150

cac aaa gtt att gat gca aca acg gct gca ttc ttt gtt aag aac tgg 534
His Lys Val Ile Asp Ala Thr Thr Ala Ala Phe Phe Val Lys Asn Trp
155 160 165

ggt gta att gct cgt ggt gct gga gaa att aag gac gtg atc att gat 582
Gly Val Ile Ala Arg Gly Ala Gly Glu Ile Lys Asp Val Ile Ile Asp
170 175 180

cat gct tcc ctg ttt ccc gca aga gat tta tcg tgc tta aca aag agt 630
His Ala Ser Leu Phe Pro Ala Arg Asp Leu Ser Cys Leu Thr Lys Ser
185 190 195

ggt gac gaa gag ttt ttg aag cca gag tct gaa aca aag cgc ttt gtg 678
Val Asp Glu Glu Phe Leu Lys Pro Glu Ser Glu Thr Lys Arg Phe Val
200 205 210 215

ttt gat ggt gcc act ata gct tct tta caa gaa acg ttt gca agt ttt 726
Phe Asp Gly Ala Thr Ile Ala Ser Leu Gln Glu Thr Phe Ala Ser Phe
220 225 230

gaa cga cgt cca aca cgc ttt gag gtt gtg tca gca gtt att ttg ggt 774
Glu Arg Arg Pro Thr Arg Phe Glu Val Val Ser Ala Val Ile Leu Gly
235 240 245

gct ttg ata act gca acg aga gaa tct gat gat gag tct aac gtt cct 822
 Ala Leu Ile Thr Ala Thr Arg Glu Ser Asp Asp Glu Ser Asn Val Pro
 250 255 260

gaa cgt ttg gac acg ata att tca gtg aat cta cgg cag aga atg aat 870
 Glu Arg Leu Asp Thr Ile Ile Ser Val Asn Leu Arg Gln Arg Met Asn
 265 270 275

cca cca ttc ccg gag cat tgc atg ggg aat ata ata tcc ggg gga tta 918
 Pro Pro Phe Pro Glu His Cys Met Gly Asn Ile Ile Ser Gly Gly Leu
 280 285 290 295

gtg tat tgg cca ctg gag aaa aaa gtt gat tac ggg tgt tta gca aaa 966
 Val Tyr Trp Pro Leu Glu Lys Lys Val Asp Tyr Gly Cys Leu Ala Lys
 300 305 310

gag att cat gaa tca ata aag aaa gtg gac gat caa ttt gcg agg aag 1014
 Glu Ile His Glu Ser Ile Lys Lys Val Asp Asp Gln Phe Ala Arg Lys
 315 320 325

ttc tat ggg gac gca gag ttc ttg aac ctg ccg agg ctt gcg ggt gct 1062
 Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala
 330 335 340

gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act 1110
 Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr
 345 350 355

ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc 1158
 Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly
 360 365 370 375

aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat 1206
 Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp
 380 385 390

ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct 1254
 Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala
 395 400 405

cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca 1302
 Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro
 410 415 420

agc ata ttt tgagggttta ttatttttt attgcactgt ttgttatttg 1351
 Ser Ile Phe
 425

tactggcttg ctgggaacat attctggcaa atttcgctga tgcaagtatc attctccata 1411

aaaatgtcaa aaaaaaaaaa aaaaa 1436

<210> 17
 <211> 1648
 <212> DNA
 <213> Citrus limon

<220>
 <221> CDS
 <222> (52)..(1524)
 <223> cDNA

<220>
 <223> Lemon acyl transferase

<400> 17
 gctaggctgg ctttcattta gcttccatct ctttctctct gtcaataact c atg gct 57
 Met Ala
 1

gca att gaa aac aga gta aca cta aag aag cat gag gtt acc aaa gtc 105
 Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val
 5 10 15

acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat 153
 Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp
 20 25 30

ctc acc tat ttc gac ttt ttc tgg ttc aag aat cct cct gtg gaa cgc 201
 Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg
 35 40 45 50

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg 249
 Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser
 55 60 65

gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat 297
Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu Leu His
70 75 80

tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag 345
Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala Ala Lys
85 90 95

cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca 393
Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser Phe Ala
100 105 110

gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc 441
Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His Leu Ser
115 120 125 130

ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag 489
Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val Pro Gln
135 140 145

ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca 537
Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln Ile Thr
150 155 160

ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca 585
Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His His Ala
165 170 175

att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat 633
Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp Ala Tyr
180 185 190

ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa 681
Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser Pro Glu
195 200 205 210

cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag 729
Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr Gly Gln
215 220 225

gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat 777
Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn Ser Asp
230 235 240

ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag 825
 Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp Ser Glu
 245 250 255

tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat 873
 Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg Glu Asp
 260 265 270

att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca 921
 Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys Ser Ser
 275 280 285 290

aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat 969
 Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu Ala Tyr
 295 300 305

gtg ttt gtt tgc atg gct aaa gct aaa tta gcc aaa gcc aaa act gaa 1017
 Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys Thr Glu
 310 315 320

gct gaa gct gca gca ggt aat gat gaa att aaa aat att att gtg gga 1065
 Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile Val Gly
 325 330 335

ttc act gcg gat tat agg agc cgt ttg gat cct cca att cca ctt aat 1113
 Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro Leu Asn
 340 345 350

tat ttt ggt aac tgc aat ggg aga cat tgt gag act gca aaa gca agt 1161
 Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys Ala Ser
 355 360 365 370

gat ttc gtt caa gaa aat ggg gtt gct ttt gtt gca gag atg tta agt 1209
 Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met Leu Ser
 375 380 385

gat atg gtc aaa ggg atc gat gcg gat gcc att gaa gcc aat gat gat 1257
 Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn Asp Asp
 390 395 400

aag gtt tca gaa ata ttg gaa att ctg aaa gaa gga gca atg att ttt 1305
 Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met Ile Phe
 405 410 415

tct gtg gct ggc tcg acc caa ttt gat gtt tac ggg tcg gat ttc ggg 1353
 Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp Phe Gly
 420 425 430

tgg ggg agg ccc aag aag gtg gag att gtg tca ata gat agg aca caa 1401
 Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg Thr Gln
 435 440 445 450

gcc atc tct ttg gca gag aga aga gat gga gga ggc ggc gtt gag gtt 1449
 Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val Glu Val
 455 460 465

gga gtt gtt tta gag aag caa caa atg gag gtt ttt gaa tct gta ttt 1497
 Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser Val Phe
 470 475 480

gct gat gga ctg aaa aat gat ctt gtt taattaatga tgtatcatct 1544
 Ala Asp Gly Leu Lys Asn Asp Leu Val
 485 490

aaatttctca atatattatt ggatcatattc aaaagaaata aattattgcg gattttgtg 1604

accaccaaatt aaaatactct tttttgaaaa aaaaaaaaaa aaaa 1648

<210> 18
 <211> 1520
 <212> DNA
 <213> Citrus limon

<220>
 <221> CDS
 <222> (4)..(1344)
 <223> cDNA

<220>
 <223> Lemon acyl transferase

<400> 18
 aac atg gca gca agc tca ctg cat ggc aaa gaa gct aca gtt ata tat 48
 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr
 1 5 10 15

cct tct gag cca acc cca tct acg gtt ttg tct ctc tca gct ctt gat 96

Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp
20 25 30

tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga 144
Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg
35 40 45

cct cgc cct ggt ttg gac cca ctt gct acc gtg gct cgt gtc aag tcc 192
Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser
50 55 60

gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc 240
Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val
65 70 75

aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc 288
Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly
80 85 90 95

caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc 336
Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr
100 105 110

gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg 384
Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu
115 120 125

tcg tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt 432
Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val
130 135 140

cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt 480
Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe
145 150 155

aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg 528
Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu
160 165 170 175

ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat 576
Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His
180 185 190

tct ctg ccg aaa ccc gtt tgg gat cgc cac cta atg aac tcc tcc tca 624
 Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser
 195 200 205

tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg 672
 Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu
 210 215 220

gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc 720
 Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser
 225 230 235

aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta 768
 Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu
 240 245 250 255

aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg 816
 Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu
 260 265 270

gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg 864
 Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp
 275 280 285

gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt 912
 Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe
 290 295 300

agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat 960
 Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr
 305 310 315

tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat 1008
 Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp
 320 325 330 335

ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg 1056
 Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala
 340 345 350

aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg 1104
 Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val
 355 360 365

agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg 1152
 Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser
 370 375 380

cag tgg tca agg cta ggg tta gag aga gtt gac ttg ggg atg ggg agg 1200
 Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg
 385 390 395

ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta 1248
 Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu
 400 405 410 415

ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc 1296
 Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro
 420 425 430

aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg 1344
 Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445

tgaggaccac accgcatgat gacccaccca tgtaatacgt tgacttataa actcagtttg 1404

acttttaact ttttaacaa gtgatggaat ttcagtgatt gactcatcac ttgatcctg 1464

atccaataaa taattgaatt gagtcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1520

<210> 19

<211> 455

<212> PRT

<213> *Fragaria vesca*

<223> Strawberry vesca alcohol acyl transferase

<400> 19

Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
 1 5 10 15

Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
 20 25 30

Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
 35 40 45

Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His

50 55 60
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 65 70 75 80
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
 85 90 95
 Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
 100 105 110
 Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
 115 120 125
 Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
 130 135 140
 Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
 145 150 155 160
 Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe
 165 170 175
 Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
 180 185 190
 Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
 195 200 205
 Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
 210 215 220
 Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
 225 230 235 240
 Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
 245 250 255
 Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
 260 265 270
 Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
 275 280 285

Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
290 295 300

Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
340 345 350

Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
355 360 365

Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
370 375 380

Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
385 390 395 400

Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
405 410 415

Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
420 425 430

Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
435 440 445

Lys Thr Leu Ile Ser Arg Tyr
450 455

<210> 20

<211> 419

<212> PRT

<213> Musa sp.

<223> Banana alcohol acyl transferase

<400> 20

Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
1 5 10 15

Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
20 25 30

Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
35 40 45

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60

Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80

Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95

Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110

Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140

Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160

Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175

Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
195 200 205

Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
210 215 220

Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
225 230 235 240

Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn

245 250 255
 Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
 260 265 270
 His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
 275 280 285
 Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
 290 295 300
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
 305 310 315 320
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
 325 330 335
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
 340 345 350
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
 355 360 365
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
 370 375 380
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
 385 390 395 400
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415

Gly Phe Ala

<210> 21

<211> 454

<212> PRT

<213> Malus sp.

<223> Apple alcohol acyl transferase

<400> 21

Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
 1 5 10 15

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
20 25 30

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
35 40 45

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
50 55 60

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
65 70 75 80

Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
85 90 95

Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
100 105 110

Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu
115 120 125

Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu
130 135 140

Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg
145 150 155 160

Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr
165 170 175

Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro
180 185 190

Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr
195 200 205

Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser
210 215 220

Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe
225 230 235 240

Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu

245	250	255
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys		
260	265	270
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val		
275	280	285
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro		
290	295	300
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys		
305	310	315 320
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val		
325	330	335
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala		
340	345	350
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser		
355	360	365
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn		
370	375	380
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp		
385	390	395 400
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile		
405	410	415
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln		
420	425	430
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn		
435	440	445
Leu Arg Ser Thr Ser Gln		
450		

<210> 22

<211> 431

<212> PRT

<213> *Mangifera indica*

<223> Mango alcohol acyl transferase

<400> 22

Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu

1 5 10 15

Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro

20 25 30

Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile

35 40 45

Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu

50 55 60

Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly

65 70 75 80

Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala

85 90 95

Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu

100 105 110

Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser

115 120 125

Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly

130 135 140

Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser

145 150 155 160

Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp

165 170 175

Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp

180 185 190

Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro

195 200 205

Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
210 215 220

Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
225 230 235 240

Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
245 250 255

Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
260 265 270

Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
275 280 285

Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
290 295 300

Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
305 310 315 320

Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
325 330 335

Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
340 345 350

Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
355 360 365

Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
370 375 380

Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
385 390 395 400

Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
405 410 415

Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
420 425 430

<210> 23

<211> 426
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase

<400> 23

Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
 1 5 10 15

Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu
 20 25 30

Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Leu Tyr Ser Lys Ala Gly
 35 40 45

Glu Ser Thr Ala Lys Thr Ser Asp His Leu Lys Glu Ser Leu Ser Asn
 50 55 60

Thr Leu Thr His Tyr Tyr Pro Leu Ala Gly Gln Leu Lys Tyr Asp Gln
 65 70 75 80

Leu Ile Val Asp Cys Asn Asp Gln Gly Val Pro Phe Ile Glu Ala His
 85 90 95

Val Thr Asn Asp Met Arg Gln Leu Leu Lys Ile Pro Asn Ile Asp Val
 100 105 110

Leu Glu Gln Leu Leu Pro Phe Lys Pro His Glu Gly Phe Asp Ser Asp
 115 120 125

Arg Ser Asn Leu Thr Val Gln Val Asn Tyr Phe Gly Cys Glu Gly Met
 130 135 140

Ala Ile Gly Leu Cys Phe Arg His Lys Val Ile Asp Ala Thr Thr Ala
 145 150 155 160

Ala Phe Phe Val Lys Asn Trp Gly Val Ile Ala Arg Gly Ala Gly Glu
 165 170 175

Ile Lys Asp Val Ile Ile Asp His Ala Ser Leu Phe Pro Ala Arg Asp
 180 185 190

Leu Ser Cys Leu Thr Lys Ser Val Asp Glu Glu Phe Leu Lys Pro Glu

195	200	205
Ser Glu Thr Lys Arg Phe Val Phe Asp Gly Ala Thr Ile Ala Ser Leu		
210	215	220
Gln Glu Thr Phe Ala Ser Phe Glu Arg Arg Pro Thr Arg Phe Glu Val		
225	230	235 240
Val Ser Ala Val Ile Leu Gly Ala Leu Ile Thr Ala Thr Arg Glu Ser		
245	250	255
Asp Asp Glu Ser Asn Val Pro Glu Arg Leu Asp Thr Ile Ile Ser Val		
260	265	270
Asn Leu Arg Gln Arg Met Asn Pro Pro Phe Pro Glu His Cys Met Gly		
275	280	285
Asn Ile Ile Ser Gly Gly Leu Val Tyr Trp Pro Leu Glu Lys Lys Val		
290	295	300
Asp Tyr Gly Cys Leu Ala Lys Glu Ile His Glu Ser Ile Lys Lys Val		
305	310	315 320
Asp Asp Gln Phe Ala Arg Lys Phe Tyr Gly Asp Ala Glu Phe Leu Asn		
325	330	335
Leu Pro Arg Leu Ala Gly Ala Glu Asp Val Lys Lys Arg Glu Phe Trp		
340	345	350
Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp		
355	360	365
Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr		
370	375	380
Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly		
385	390	395 400
Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu		
405	410	415
Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe		
420	425	

<210> 24
 <211> 491
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase

<400> 24

Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
 1 5 10 15

Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
 20 25 30

Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val
 35 40 45

Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
 50 55 60

Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
 65 70 75 80

Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
 85 90 95

Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
 100 105 110

Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
 115 120 125

Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
 130 135 140

Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
 145 150 155 160

Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
 165 170 175

His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
 180 185 190

Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
195 200 205

Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr
210 215 220

Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn
225 230 235 240

Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp
245 250 255

Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg
260 265 270

Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys
275 280 285

Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu
290 295 300

Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys
305 310 315 320

Thr Glu Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile
325 330 335

Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro
340 345 350

Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys
355 360 365

Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met
370 375 380

Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn
385 390 395 400

Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met
405 410 415

Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp

420 425 430
 Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg
 435 440 445
 Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val
 450 455 460
 Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser
 465 470 475 480
 Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val
 485 490

<210> 25
 <211> 447
 <212> PRT
 <213> Citrus limon
 <223> Lemon acyl transferase

<400> 25
 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro
 1 5 10 15
 Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser
 20 25 30
 Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro
 35 40 45
 Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala
 50 55 60
 Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg
 65 70 75 80
 Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln
 85 90 95
 Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp
 100 105 110
 Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser

115	120	125	
Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln			
130	135	140	
Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn			
145	150	155	160
His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe			
165	170	175	
Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His Ser			
180	185	190	
Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser			
195	200	205	
Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu			
210	215	220	
Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn			
225	230	235	240
Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn			
245	250	255	
Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala			
260	265	270	
Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala			
275	280	285	
Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser			
290	295	300	
Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr			
305	310	315	320
Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu			
325	330	335	
Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys			
340	345	350	

Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
355 360 365

His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
370 375 380

Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
385 390 395 400

Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
405 410 415

Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
420 425 430

Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
435 440 445

<210> 26

<211> 456

<212> PRT

<213> Cucumis melo

<223> Honey dew melon alcohol acyl transferase

<400> 26

Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
1 5 10 15

Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
20 25 30

Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
35 40 45

His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
50 55 60

Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
65 70 75 80

Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
85 90 95

Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
 130 135 140
 Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
 145 150 155 160
 Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
 165 170 175
 Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
 180 185 190
 Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe
 195 200 205
 Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile
 210 215 220
 Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln
 225 230 235 240
 Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro
 245 250 255
 Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala
 260 265 270
 Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn
 275 280 285
 Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val
 290 295 300
 Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro
 305 310 315 320
 Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr

325 330 335
 Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg
 340 345 350
 Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg
 355 360 365
 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
 370 375 380
 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
 385 390 395 400
 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
 405 410 415
 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
 420 425 430
 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
 435 440 445
 Gln Thr Ile Gln Ser Ala Ser Lys
 450 455

<210> 27

<211> 397

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry aminotransferase

<400> 27

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg
 1 5 10 15

Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu
 20 25 30

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
 35 40 45

Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly

50 55 60
 Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
 65 70 75 80
 Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
 85 90 95
 Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
 100 105 110
 Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
 115 120 125
 Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
 130 135 140
 Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
 145 150 155 160
 Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
 165 170 175
 Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
 180 185 190
 Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
 195 200 205
 Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
 210 215 220
 Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
 225 230 235 240
 Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
 245 250 255
 Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
 260 265 270
 Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
 275 280 285

Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
290 295 300

Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
305 310 315 320

Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
325 330 335

Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
340 345 350

Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
355 360 365

Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
370 375 380

Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
385 390 395

<210> 28

<211> 458

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry thiolase

<400> 28

Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
1 5 10 15

Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
20 25 30

Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
35 40 45

Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
50 55 60

Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
65 70 75 80

Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
85 90 95

Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
100 105 110

Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
115 120 125

Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
130 135 140

Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
145 150 155 160

Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
165 170 175

Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
180 185 190

Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
195 200 205

Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
210 215 220

Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
225 230 235 240

Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
245 250 255

Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu
260 265 270

Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser
275 280 285

Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val
290 295 300

Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val

305 310 315 320
 Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala
 325 330 335
 Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp
 340 345 350
 Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg
 355 360 365
 Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala
 370 375 380
 Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala
 385 390 395 400
 Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly
 405 410 415
 Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Ala Val Phe
 420 425 430
 Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu
 435 440 445
 Ser Leu Asn Phe Leu Ser Lys Asp Val Arg
 450 455
 <210> 29
 <211> 605
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry pyruvate decarboxylase
 <400> 29
 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
 1 5 10 15
 Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
 20 25 30
 Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His

35	40	45	
Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val			
50	55	60	
Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro			
65	70	75	80
Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala			
85	90	95	
Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr			
100	105	110	
Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr			
115	120	125	
Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn			
130	135	140	
Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp			
145	150	155	160
Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala			
165	170	175	
Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile			
180	185	190	
Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys			
195	200	205	
Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro			
210	215	220	
Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala			
225	230	235	240
Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met			
245	250	255	
Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val			
260	265	270	

Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
275 280 285

Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
290 295 300

Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
305 310 315 320

Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
325 330 335

Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
340 345 350

Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
355 360 365

Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
370 375 380

His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
385 390 395 400

Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
405 410 415

Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
420 425 430

Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
435 440 445

Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
450 455 460

Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
465 470 475 480

Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
485 490 495

Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr

500 505 510
 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
 515 520 525
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
 530 535 540
 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
 545 550 555 560
 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
 565 570 575
 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
 580 585 590
 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
 595 600 605

<210> 30
 <211> 333
 <212> PRT
 <213> Fragaria x ananassa
 <223> Strawberry alcohol dehydrogenase

<400> 30
 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
 1 5 10 15
 Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
 20 25 30
 Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
 35 40 45
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
 50 55 60

Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
65 70 75 80

Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
 85 90 95

Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
 100 105 110

Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
 115 120 125

Tyr Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
 130 135 140

Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
145 150 155 160

Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
 165 170 175

Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
 180 185 190

Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
 195 200 205

Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg
 210 215 220

Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
225 230 235 240

Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
 245 250 255

Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
 260 265 270

Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
 275 280 285

Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly

290 295 300
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
 305 310 315 320
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330
 <210> 31
 <211> 326
 <212> PRT
 <213> *Fragaria x ananassa*
 <223> Strawberry alcohol dehydrogenase
 <400> 31
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
 1 5 10 15
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
 20 25 30
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
 35 40 45
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
 50 55 60
 Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
 65 70 75 80
 Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
 85 90 95
 Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp
 100 105 110
 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
 115 120 125
 Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr
 130 135 140
 Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg

145 150 155 160
 Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser
 165 170 175
 Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr
 180 185 190
 Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp
 195 200 205
 Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val
 210 215 220
 Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn
 225 230 235 240
 Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro
 245 250 255
 Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile
 260 265 270
 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His
 275 280 285
 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr
 290 295 300
 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile
 305 310 315 320
 Asp Val Glu Asn Thr Leu
 325

<210> 32

<211> 278

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 32

Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu

1	5	10	15
Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn			
20	25	30	
Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly			
35	40	45	
Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala			
50	55	60	
Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro			
65	70	75	80
Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly			
85	90	95	
Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu			
100	105	110	
Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr			
115	120	125	
Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu			
130	135	140	
Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala			
145	150	155	160
Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His			
165	170	175	
Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val			
180	185	190	
Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu			
195	200	205	
Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys			
210	215	220	
Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala			
225	230	235	240

Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg
245 250 255

Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn
260 265 270

Thr Leu Lys Pro Ala Ile
275

<210> 33

<211> 283

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 33

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg
1 5 10 15

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile
20 25 30

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
35 40 45

Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
50 55 60

Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
65 70 75 80

Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
85 90 95

Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
100 105 110

Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
115 120 125

Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
130 135 140

Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
145 150 155 160

Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
 165 170 175

Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
 180 185 190

Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys
 195 200 205

His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
 210 215 220

Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
225 230 235 240

Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
 245 250 255

Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
 260 265 270

Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
 275 280

<210> 34

<211> 188

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 34

Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
1 5 10 15

Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
 20 25 30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
 35 40 45

Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
50 55 60

Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
65 70 75 80

Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
85 90 95

Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
100 105 110

Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
115 120 125

Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
130 135 140

Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
145 150 155 160

Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
165 170 175

Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
180 185

<210> 35

<211> 1227

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(979)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 35

g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49

Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val

1	5	10	15
---	---	----	----

tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97
Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
20 25 30

tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145
Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
35 40 45

gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193
Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
50 55 60

ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241
Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
65 70 75 80

gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac 289
Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
85 90 95

gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat 337
Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp
100 105 110

gag cac ttc att gtt cgg atc ccg gac aac tta cct ctt gat ggc gct 385
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
115 120 125

gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat 433
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr
130 135 140

tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg 481
Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg
145 150 155 160

cgg ttt agg tca cgt ccg ccg tta aat ttg cca ggg ctt tgg ggc tca 529
Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser
165 170 175

agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat 577

Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr
 180 185 190

gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat 625
 Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp
 195 200 205

cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt 673
 Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val
 210 215 220

cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat 721
 Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn
 225 230 235 240

gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca 769
 Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro
 245 250 255

gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att 817
 Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile
 260 265 270

gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat 865
 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His
 275 280 285

aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc 913
 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr
 290 295 300

gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc 961
 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile
 305 310 315 320

gac gtt gag aac aca ttg taagtccgcc taagttttc attcaattct 1009
 Asp Val Glu Asn Thr Leu
 325

gttaataaga ctatgcatta atatagact gactctccat aggatggagt tatcagtctt 1069

caaatttcta gacatatttt gtgatcaaat aaatggaatg gctttgtttt cctttccac 1129

taagattaga ttccagttgt attgtttta aagagattga tgttttatt aattgtaaca 1189

gtgttatcag tctaatacatt aaaaaaaaaa aaaaaaaaaa 1227

<210> 36

<211> 1063

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(836)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 36

gc aaa gtg caa aaa ttt aaa gtt gga gac aaa gtt ggt gtt ggg tgc 47

Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys

1 5 10 15

ttg gta ggc tca tgc aaa act tgc gac agc tgt gct aac gat ttg gag 95

Leu Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu

20 25 30

aac tac tgc ccc aaa cag ata cag act tac ggc gcc aag tac ctt gac 143

Asn Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp

35 40 45

gga aca acc aca tac ggc ggt tac tct gac atc atg gtg gcg gat gag 191

Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu

50 55 60

gcc ttt gta atc cgt att ccg gac aac ctg cct ctt gag ggt gct gct 239

Ala Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala

65 70 75

cct ctc cta tgt gcc gga atc aca act tac agt ccc ctg agg tat ttc 287

Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe

80 85 90 95

gga ctt gac aaa ccc ggc atg cat gtc ggg gtg gtt ggc ctt ggc ggt 335

Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly
100 105 110

tta ggc cat gtc gcg gtg aag ttt gcc aag gct ttg ggg gtt aat gtc 383
Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val
115 120 125

aca gtg atc agt acc tcc gct aat aag aaa gat gaa gct att aaa cac 431
Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His
130 135 140

ctt ggt gct gat tct ttc ttg gtc agt cgt gac caa gat cag atg cag 479
Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln
145 150 155

gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc 527
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val
160 165 170 175

cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt 575
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu
180 185 190

gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct 623
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser
195 200 205

tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc 671
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile
210 215 220

aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg 719
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr
225 230 235

gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag 767
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu
240 245 250 255

cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga 815
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly
260 265 270

aac aca ttg aag ccg gcc att taaattgca ttctgatcag aaactgaatc 866

Asn Thr Leu Lys Pro Ala Ile

275

aagcgaggtc gagaggccta cgtaacaatg caaacatgtg ctagcttggt ctggagtag 926

tccttagctt ttctctgatg tattccatct gttttgttca tgtcccatct tattatgaga 986

aaaatgtggg taccgtggat attgaataaa tgaagagcta ctggaacgat ggtttcacaa 1046

aaaaaaaaa aaaaaaa

1063

<210> 37

<211> 1228

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (1)..(849)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 37

gca aga gat tca tct ggt gtc ctc tct ccc ttc aat ttc tcc aga agg 48

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg

1

5

10

15

gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att 96

Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile

20

25

30

tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 144

Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr

35

40

45

tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta 192

Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val

50

55

60

ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga 240

Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
65 70 75 80

tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 288
Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
85 90 95

gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 336
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
100 105 110

gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac 384
Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
115 120 125

gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct 432
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
130 135 140

gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 480
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
145 150 155 160

ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc 528
Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
165 170 175

ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag 576
Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
180 185 190

ggt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa 624
Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys
195 200 205

cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg 672
His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
210 215 220

cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca 720
Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
225 230 235 240

caa cat cct ctc ctg cct ttg att ggt ttg aag tct cat gga aag 768
 Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
 245 250 255

ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt 816
 Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
 260 265 270

cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat 869
 Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
 275 280

gaaggagaca caagagatga tagattttgc tgccaggcac aacataacag cagacatcga 929

agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga 989

taccgttttg tcatcgacat tggaacaca ctgaaggcta gcacttaaatt tctgcaatcc 1049

agactgtatc aatgaagaaa caagaacaga aactgagatt gatttgggtgt catactccgc 1109

ctatggtttt ccttacagca tttttgttg ttgctacat gaataacgat cacatgaact 1169

gtgatgattt gataataaaa gaatacataa acaaaaaaaaa caaaaaaaaa aaaaaaaaa 1228

<210> 38

<211> 852

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(566)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 38

gt ccc ctg agg tat ttc gga ctt gac aaa ccc ggc atg cat gtc ggg 47
 Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly
 1 5 10 15

gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag 95

Val Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys
20 25 30

gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa 143
Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys
35 40 45

gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt 191
Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg
50 55 60

gac caa gat cag atg cag gct gcc atg gga aca ttg gac ggt atc atc 239
Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile
65 70 75

gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg 287
Asp Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu
80 85 90 95

aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt 335
Lys Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu
100 105 110

gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt 383
Glu Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly
115 120 125

agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca 431
Ser Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala
130 135 140

gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat 479
Ala Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr
145 150 155

ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg 527
Leu Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg
160 165 170 175

ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaattgca 576
Phe Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
180 185

tttcgatcag aaactgaatc aagcgatgac gagaggccta cgtaacaatg taaacatgtg 636

ctagcttggt cttgtagtag tctttagcat ttctctgatg tactccttct gttttgttca 696

tgttccatct tataataaga ttcttattat gaaaaaaata tggtagcgtg gatattgaat 756

aatgaagaa ctactggaac aatggtttca caaattattt gtggtgctaa aaaaaaaaaa 816

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 852

<210> 39

<211> 181

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 39

Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly

1 5 10 15

Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His

20 25 30

Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu

35 40 45

His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met

50 55 60

Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val

65 70 75 80

Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys

85 90 95

Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro

100 105 110

Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu

115 120 125

His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala

130 135 140

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
145 150 155 160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
 165 170 175

Cys Arg Gln Gln Ser
 180

<210> 40

<211> 176

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 40

Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
1 5 10 15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
65 70 75 80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125

Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140

Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
145 150 155 160

Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
 165 170 175

<210> 41

<211> 283

<212> PRT

<213> Fragaria x ananassa

<223> Strawberry alcohol dehydrogenase

<400> 41

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
1 5 10 15

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
 20 25 30

Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
 35 40 45

Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
 50 55 60

Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
65 70 75 80

Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
 85 90 95

Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
 100 105 110

Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
 115 120 125

Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
 130 135 140

Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
145 150 155 160

Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
165 170 175

Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
180 185 190

Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
195 200 205

Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
210 215 220

Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
225 230 235 240

Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
245 250 255

Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
260 265 270

Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
275 280

<210> 42

<211> 1010

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(850)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 42

g gaa act acc atc aat ttt ggg tct aag aag att gca gtt gtt act gga 49

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly

1 5 10 15

gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa 97

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
20 25 30

gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa 145
Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
35 40 45

gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat 193
Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
50 55 60

cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt 241
Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
65 70 75 80

ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga 289
Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
85 90 95

gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca 337
Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
100 105 110

tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag 385
Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
115 120 125

caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca 433
Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
130 135 140

agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga 481
Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
145 150 155 160

aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag 529
Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
165 170 175

gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag 577
Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
180 185 190

gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att 625
 Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
 195 200 205

gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag 673
 Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
 210 215 220

tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca 721
 Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
 225 230 235 240

gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta 769
 Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
 245 250 255

ggt cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc 817
 Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270

ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga 870
 Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

tgaactggac tatttttagat ttccagaatg tgcttgattt tgttgaagta tttatgggat 930

ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaaa 990

aaaaaaaaaa aaaaaaaaaa 1010

<210> 43
 <211> 243
 <212> PRT
 <213> Mangifera indica
 <223> Mango esterase

<400> 43
 Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
 1 5 10 15

Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
 20 25 30

Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45

Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
130 135 140

Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
145 150 155 160

Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
165 170 175

Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
180 185 190

Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
195 200 205

Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
225 230 235 240

Ala Glu Phe

<210> 44

<211> 877

<212> DNA

<213> Mangifera indica

<220>

<221> CDS

<222> (1)..(729)

<223> cDNA

<220>

<223> Mango esterase

<400> 44

atg agg cca caa ata gtg tta ttc gga gat tca ata acg gag caa tct 48
Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
1 5 10 15

ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc 96
Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
20 25 30

aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg 144
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45

gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct 192
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt 240
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac 288
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg 336
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa 384
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag 432
 Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
 130 135 140

agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg 480
 Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
 145 150 155 160

gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca 528
 Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
 165 170 175

gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca 576
 Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
 180 185 190

gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa 624
 Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
 195 200 205

gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca 672
 Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
 210 215 220

gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct 720
 Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
 225 230 235 240

gct gaa ttc tagtcaagac aggcttgga attgttctc tctttcaatt 769
 Ala Glu Phe

tttctatttg atgaaaagat ttggactgct ttttctagt catgccaaat gaaacagtgt 829

tagccttttg cctattttat cagatgctga tatgcgctct gtgtcgac 877

<210> 45

<211> 12

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<400> 45

Trp Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp

1 5 10

<210> 46

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<221> misc_feature

<222> (1)..(10)

<223> Xaa is any amino acid residue

<400> 46

Leu Xaa Xaa Xaa Tyr Pro Xaa Xaa Gly Arg

1 5 10

<210> 47

<211> 16

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: various fruit

<220>

<223> alcohol acyl transferase motif

<221> misc_feature

<222> (1)..(16)

<223> Xaa is any amino acid residue

<400> 47

Pro Ser Arg Val Xaa Xaa Val Thr Xaa Phe Leu Xaa Lys Xaa Leu Ile
 1 5 10 15

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <223> PCR Primer
 <220>
 <221> misc_feature
 <222>(9)..(9)
 <223> N is Inosine

<400> 48
 ggwtgggggnk ctaytcttgc 20

<210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <221>
 <222>
 <223> PCR Primer

<220>
 <223> AAP165

<400> 49
 cggatccgga gaaaattgag gtcag 25

<210> 50
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <221>
 <222>
 <223> PCR Primer

<220>

<223> AAP166

<400> 50

cgtcgacat tgcacgagcc acataatc

28